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RAW SEQUENCE LISTING

DATE: 07/03/2002

PATENT APPLICATION: US/09/929,612A

TIME: 12:45:45

Input Set : A:\-31-1-5.app

Output Set: N:\CRF3\07032002\I929612A.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Golstein, Pierre

7 Rouvier, Eric

8 Fossiez, Francois

9 Lebecque, Serge J.E.

10 Djossou, Odile

11 Banchereau, Jacques

13 (ii) TITLE OF INVENTION: Purified Mammalian CTLA-8 Antigens and
14 Related Reagents

16 (iii) NUMBER OF SEQUENCES: 10

18 (iv) CORRESPONDENCE ADDRESS:

19 (A) ADDRESSEE: Townsend and Townsend and Crew LLP

20 (B) STREET: Two Embarcadero Center, Eighth Floor

21 (C) CITY: San Francisco

22 (D) STATE: California

23 (E) COUNTRY: USA

24 (F) ZIP: 94111-3834

26 (v) COMPUTER READABLE FORM:

27 (A) MEDIUM TYPE: Floppy disk

28 (B) COMPUTER: IBM PC compatible

29 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

30 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

32 (vi) CURRENT APPLICATION DATA:

C--> 33 (A) APPLICATION NUMBER: US/09/929,612A

C--> 34 (B) FILING DATE: 13-Aug-2001

35 (C) CLASSIFICATION:

53 (vii) PRIOR APPLICATION DATA:

38 (A) APPLICATION NUMBER: US 08/077,203

39 (B) FILING DATE: 14-JUN-1993

42 (A) APPLICATION NUMBER: US 08/177,747

43 (B) FILING DATE: 05-JAN-1994

46 (A) APPLICATION NUMBER: US 08/250,846

47 (B) FILING DATE: 27-MAY-1994

50 (A) APPLICATION NUMBER: US 08/432,994

51 (B) FILING DATE: 02-MAY-1995

54 (A) APPLICATION NUMBER: US 08/432,994

55 (B) FILING DATE: 22-JUN-1998

57 (viii) ATTORNEY/AGENT INFORMATION:

58 (A) NAME: Weber, Kenneth A.

59 (B) REGISTRATION NUMBER: 31,677

60 (C) REFERENCE/DOCKET NUMBER: 015631-003115US

62 (ix) TELECOMMUNICATION INFORMATION:

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63      (A) TELEPHONE: (415) 576-0200
64      (B) TELEFAX: (415) 576-0300
67 (2) INFORMATION FOR SEQ ID NO: 1:
69      (i) SEQUENCE CHARACTERISTICS:
70          (A) LENGTH: 1080 base pairs
71          (B) TYPE: nucleic acid
72          (C) STRANDEDNESS: single
73          (D) TOPOLOGY: linear
75      (ii) MOLECULE TYPE: cDNA
78      (ix) FEATURE:
79          (A) NAME/KEY: CDS
80          (B) LOCATION: 12..464
81          (D) OTHER INFORMATION: /product= "mouse/rat CTLA-8"
84      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
86 GAATTCATC C ATG TGC CTG ATG CTG TTG CTG CTA CTG AAC CTG GAG GCT      50
87      Met Cys Leu Met Leu Leu Leu Leu Leu Leu Glu Ala
88      1 5 10
90 ACA GTG AAG GCA GCG GTA CTC ATC CCT CAA AGT TCA GTG TGT CCA AAC      98
91 Thr Val Lys Ala Ala Val Leu Ile Pro Gln Ser Ser Val Cys Pro Asn
92 15 20 25
94 GCC GAG GCC AAT AAC TTT CTC CAG AAC GTG AAG GTC AAC CTG AAA GTC      146
95 Ala Glu Ala Asn Asn Phe Leu Gln Asn Val Lys Val Asn Leu Lys Val
96 30 35 40 45
98 ATC AAC TCC CTT AGC TCA AAA GCG AGC TCC AGA AGG CCC TCA GAC TAC      194
99 Ile Asn Ser Leu Ser Ser Lys Ala Ser Ser Arg Arg Pro Ser Asp Tyr
100 50 55 60
102 CTC AAC CGT TCC ACT TCA CCC TGG ACT CTG AGC CGC AAT GAG GAC CCT      242
103 Leu Asn Arg Ser Thr Ser Pro Trp Thr Leu Ser Arg Asn Glu Asp Pro
104 65 70 75
106 GAT AGA TAT CCT TCT GTG ATC TGG GAG GCA CAG TGC CGC CAC CAG CGC      290
107 Asp Arg Tyr Pro Ser Val Ile Trp Glu Ala Gln Cys Arg His Gln Arg
108 80 85 90
110 TGT GTC AAC GCT GAG GGG AAG TTG GAC CAC CAC ATG AAT TCT GTT CTC      338
111 Cys Val Asn Ala Glu Gly Lys Leu Asp His His Met Asn Ser Val Leu
112 95 100 105
114 ATC CAG CAA GAG ATC CTG GTC CTG AAG AGG GAG CCT GAG AAG TGC CCC      386
115 Ile Gln Gln Glu Ile Leu Val Leu Lys Arg Glu Pro Glu Lys Cys Pro
116 110 115 120 125
118 TTC ACT TTC CGG GTG GAG AAG ATG CTG GTG GGC GTG GGC TGC ACC TGC      434
119 Phe Thr Phe Arg Val Glu Lys Met Leu Val Gly Val Gly Cys Thr Cys
120 130 135 140
122 GTT TCC TCT ATT GTC CGC CAT GCG TCC TAAACAGAGA CCTGAGGCTA      481
123 Val Ser Ser Ile Val Arg His Ala Ser
124 145 150
126 GCCCCTAAGA AACCCCTGCG TTTCTCTGCA AACTTCCTTG TCTTTTAAAA ACAGTTCACA      541
128 GTTGAATCTC AGCAAGTGAT ATGGATTTAA AGGCGGGGTT AGAATTGTCT GCCTTCCACC      601
130 CTGAAAAGAA GGCGCAGAGG GGATATAAAT TGCTTCTTGT TTTTCTGTGG GCTTTAAATT      661
132 ATTTATGTAT TTAATCTATC CCGAGATAAC TTTGAGGCAT AAGTTATTTT AATGAATTAT      721
134 CTACATTATT ATTATGTTTC TTAATGCAGA AGACAAAATT CAAGACTAAG AAATTTTATT      781

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136 ATTTAAAAGG TAAAACCTAT ATTTATATGA GCTATTTATG GGTCTATTTA TTTTCTTCA      841
138 GTGCTAAGAT CATGATTATC AGATCTACCT AAGGAAGTCC TAAATAATAT TAAATATTAA      901
140 TTGAAATTC AGTTTACTA TTTGCTTATT TAAGGTTCCC ICCTCTGAAT GGTGTGAAAT      961
142 CAAACCTCGT TTTATGTTT TAAATTATTG AGGCTTCGAA AAATTGGGCA ATTTAGCTTC      1021
144 CTACTGTGTG TTTAAAAACC TTGTAACAAT ATCACTATAA TAAATTTTGT GAAGAAAAAT      1080

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147 (2) INFORMATION FOR SEQ ID NO: 2:

149 (i) SEQUENCE CHARACTERISTICS:

150 (A) LENGTH: 150 amino acids

151 (B) TYPE: amino acid

152 (D) TOPOLOGY: linear

154 (ii) MOLECULE TYPE: protein

156 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

158 Met Cys Leu Met Leu Leu Leu Leu Asn Leu Glu Ala Thr Val Lys

159 1 5 10 15

161 Ala Ala Val Leu Ile Pro Gln Ser Ser Val Cys Pro Asn Ala Glu Ala

162 20 25 30

164 Asn Asn Phe Leu Gln Asn Val Lys Val Asn Leu Lys Val Ile Asn Ser

165 35 40 45

167 Leu Ser Ser Lys Ala Ser Ser Arg Arg Pro Ser Asp Tyr Leu Asn Arg

168 50 55 60

170 Ser Thr Ser Pro Trp Thr Leu Ser Arg Asn Glu Asp Pro Asp Arg Tyr

171 65 70 75 80

173 Pro Ser Val Ile Trp Glu Ala Gln Cys Arg His Gln Arg Cys Val Asn

174 85 90 95

176 Ala Glu Gly Lys Leu Asp His His Met Asn Ser Val Leu Ile Gln Gln

177 100 105 110

179 Glu Ile Leu Val Leu Lys Arg Glu Pro Glu Lys Cys Pro Phe Thr Phe

180 115 120 125

182 Arg Val Glu Lys Met Leu Val Gly Val Gly Cys Thr Cys Val Ser Ser

183 130 135 140

185 Ile Val Arg His Ala Ser

186 145 150

189 (2) INFORMATION FOR SEQ ID NO: 3:

191 (i) SEQUENCE CHARACTERISTICS:

192 (A) LENGTH: 2520 base pairs

193 (B) TYPE: nucleic acid

194 (C) STRANDEDNESS: single

195 (D) TOPOLOGY: linear

197 (ii) MOLECULE TYPE: DNA (genomic)

200 (ix) FEATURE:

201 (A) NAME/KEY: CDS

202 (B) LOCATION: 1574..2029

203 (D) OTHER INFORMATION: /product= "Saimiriine herpesvirus 2

204 immediate-early protein"

205 /note= "open reading frame 2 (ORF2)"

208 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

210 AGCTTCATGC AAATACATCT TATCTTACCA GATTCTCGCC TCATTGCAA ACATGCCTCA 60

212 TCTTTTGAGA AGAAACGCAA TTCGAAGCTT TTCTAATGCT CCTGAAGAGC AGCCTGTGCT 120

214 GCAGCCTGAG CTTGATGCTA TTGAAGAGCT AGAATAAGAG CTATTTTGTG ACGATGGGTG 180

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216	CTGCCTTTCT	GTTCAAGAAA	TCTGCTTAAT	TGTTCTTGGA	TTCTTATTGT	TTCTGCTAGC	240
218	TGTAATTGTT	TTTTATAACT	ATACAGACAC	AGATCAATTT	GTGAAGCTGA	CACATCTTAT	300
220	GAGCCACAAA	AATTCTATCA	AAGGACCTTT	TGATCTTTAA	GGTATGTACT	CATAATTTTA	360
222	TTTTTTTATT	TCTAAAACAA	TCTTAGTATA	TATAATTAAT	ACAAATTTTA	GAAAATACTA	420
224	TAATAAATAT	TGAAAGCTGT	ATTTACATTG	TAAACTATAT	ATAGGCAATG	TAAAGTCATT	480
226	CTAACCTTAG	GTTTGCTTTA	CCTGTTACAG	AAACTTCACC	TGTGTGTCAA	GAGCTGCAAA	540
228	CATGGCTTTA	GACTTAAGAA	ATCTTAAACA	CCTGACTGCT	AACTTCAGTT	TTAGAATAAT	600
230	GATATGGATT	ATGCTATGTT	TGGCTCTACC	TACTGATAGT	AAACCTATTT	CAACAACCTGA	660
232	AGCTCCAATA	CTAAACATAA	CACAATCTCC	AAGTTTGAAC	ATCTCATCAC	CTTCTACTTT	720
234	AGAACCTTCA	GAGCCTCTTA	AAAACCTGTAC	AACATTCTTA	GACTTACTTT	GGCAGCGGCT	780
236	GGGCGAGAAC	GCTTCTATAA	AGGACTTGAT	GTTAACATTA	CAACGAGAAG	AAGTCCACGG	840
238	AAGAATGACT	ACACTTCCTT	CACCTAGACC	AAGCAGTAAA	GTTGAAGAAC	AACAGTTACA	900
240	AAGACCTAGA	AACTTACTGC	CTACTGCTGT	CGGGCCACCT	CATGTCAAAT	ATAGACTATA	960
242	TAATCGCTTA	TGGGAAGCTC	CTAAAGGAGC	TGATGTTAAT	GGTAAACCTA	TACAATTTGA	1020
244	TGACCCTCCT	CTTCCTTATA	CAGGGGCATA	TAATGATGAT	GGTGTTTTAA	TGGTTAATAT	1080
246	TAATGGAAAA	CATGTGAGGT	TTGATAGCIT	GTCTTATTGG	GAAAGAATTA	AAAGATCTGG	1140
248	TACCCCATGG	TGTATAAAGA	CACCAAGTGA	AAAAGCAGCA	ATATTGAAGC	AGCTTTTAAA	1200
250	AGCTGAAAAA	AAATGTAGGA	CTACTTCTAA	ACGTATCACT	GAGTTAGAAG	AGCAGATTAA	1260
252	AGAACTAGAA	AAAAC TAGTA	CATCTCCATA	GATTACTGTT	AGAATGTGTT	TATCATACTA	1320
254	AAATAAATGC	TTTATGTATT	GCAATATTAC	TTGTTTGCTA	TGACTTTGGT	ATATGAAATG	1380
256	CAAATCTTAA	ATAAAAAGTT	TTTGTCTAGT	ATTGGCGTCA	CTGTATTTTA	CTAGCAAAAA	1440
258	TATATAAATT	GTTATGTAGC	AAGAAGTTTG	TATCAATATA	AAAAC TCTAA	AGTATATAAA	1500
260	CAAACATTCA	ATTAGTGTA	ATCATAGCAA	GCATATCTTT	TCATACGTGT	CTAGTTAATT	1560
262	TAAAGAATTA	ATT ATG ACA	TTT AGA	ATG ACT	TCA CTT	GTG TTA CTT CTG	1609
263		Met Thr Phe Arg	Met Thr Ser	Leu Val Leu	Leu Leu		
264		1	5	10			
266	CTG CTG AGC	ATA GAT TGT	ATA GTA AAG	TCA GAA	ATA ACA AGC	GCA CAA	1657
267	Leu Leu Ser	Ile Asp Cys	Ile Val Lys	Ser Glu	Ile Thr Ser	Ala Gln	
268		15	20	25			
270	ACC CCA AGA	TGC TTA GCT	GCT AAC AAT	AGC TTT	CCA CGG	TCT GTG	ATG
271	Thr Pro Arg	Cys Leu Ala	Ala Asn Asn	Ser Phe	Pro Arg Ser	Val Met	
272		30	35	40			
274	GTT ACT TTG	AGC ATC CGT	AAC TGG	AAT ACT	AGT TCT	AAA AGG	GCT TCA
275	Val Thr Leu	Ser Ile Arg	Asn Trp	Asn Thr	Ser Ser	Lys Arg	Ala Ser
276	45	50	55	60			
278	GAC TAC TAC	AAT AGA TCT	ACG TCT	CCT TGG	ACT CTC	CAT CGC	AAT GAA
279	Asp Tyr Tyr	Asn Arg Ser	Thr Ser	Pro Trp	Thr Leu	His Arg	Asn Glu
280		65	70	75			
282	GAT CAA GAT	AGA TAT CCC	TCT GTG	ATT TGG	GAA GCA	AAG TGT	CGC TAC
283	Asp Gln Asp	Arg Tyr Pro	Ser Val Ile	Trp Glu	Ala Lys	Cys Arg	Tyr
284		80	85	90			
286	TTA GGA TGT	GTT AAT GCT	GAT GGG	AAT GTA	GAC TAC	CAC ATG	AAC TCA
287	Leu Gly Cys	Val Asn Ala	Asp Gly	Asn Val	Asp Tyr	His Met	Asn Ser
288		95	100	105			
290	GTC CCT ATC	CAA CAA GAG	ATT CTA	GTG GTG	CGC AAA	GGG CAT	CAA CCC
291	Val Pro Ile	Gln Gln Glu	Ile Leu	Val Val	Arg Lys	Gly His	Gln Pro
292		110	115	120			
294	TGC CCT AAT	TCA TTT AGG	CTA GAG	AAG ATG	CTA GTG	ACT GTA	GGC TGC
295	Cys Pro Asn	Ser Phe Arg	Leu Glu	Lys Met	Leu Val	Thr Val	Gly Cys

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296 125          130          135          140
298 ACA TGC GTT ACT CCC ATT GTT CAC AAT GTA GAC TAAAAGCTAT CTAAATTTTG 2046
299 Thr Cys Val Thr Pro Ile Val His Asn Val Asp
300          145          150
302 AAAATTAACA TTTCATAAA AAACAAAAAC TTGATTTTTT TCTTTTAAAT AAAAAAAGTT 2106
304 TAATATAAGT TCTGGCTTGT TTGGTTTTTG ACTAATCAAT GTAGATCACA CTTGTGATCT 2166
306 TAGCTCTCGG GAAGCAATGT AAGAAAATAT ATTTAACTTA AGAGTTTATAG ACTTGCTTGA 2226
308 GTTTTATGAG TAAAAAACAA AGAATAAGCA CAGCTTCTTG TATCTTCTTT TAAAAACTTT 2286
310 AAGTTATTTA TGTATTTAAT ATAATCTAAT GTTCTTTAAA CATGTTGAGT TTGAGGTOCA 2346
312 CTAATACAAC ATTATAATTT TTTCTGTTAT AACACTTTTG CAAGAAGAAC TCATTTTATA 2406
314 GAAAATGAGC AGTATTCAAA AAAAATGTTT GATATGCTGT AATATTGGAG AGGAAGAAGT 2466
316 TTTACAAGCA TGTGATTGTC CTAGCAGAGT CCATCATACA TGCTTACAAA GTCA 2520

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319 (2) INFORMATION FOR SEQ ID NO: 4:

321 (i) SEQUENCE CHARACTERISTICS:

322 (A) LENGTH: 151 amino acids

323 (B) TYPE: amino acid

324 (D) TOPOLOGY: linear

326 (ii) MOLECULE TYPE: protein

328 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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330 Met Thr Phe Arg Met Thr Ser Leu Val Leu Leu Leu Ser Ile
331 1          5          10          15
333 Asp Cys Ile Val Lys Ser Glu Ile Thr Ser Ala Gln Thr Pro Arg Cys
334          20          25          30
336 Leu Ala Ala Asn Asn Ser Phe Pro Arg Ser Val Met Val Thr Leu Ser
337          35          40          45
339 Ile Arg Asn Trp Asn Thr Ser Ser Lys Arg Ala Ser Asp Tyr Tyr Asn
340          50          55          60
342 Arg Ser Thr Ser Pro Trp Thr Leu His Arg Asn Glu Asp Gln Asp Arg
343 65          70          75          80
345 Tyr Pro Ser Val Ile Trp Glu Ala Lys Cys Arg Tyr Leu Gly Cys Val
346          85          90          95
348 Asn Ala Asp Gly Asn Val Asp Tyr His Met Asn Ser Val Pro Ile Gln
349          100          105          110
351 Gln Glu Ile Leu Val Val Arg Lys Gly His Gln Pro Cys Pro Asn Ser
352          115          120          125
354 Phe Arg Leu Glu Lys Met Leu Val Thr Val Gly Cys Thr Cys Val Thr
355          130          135          140
357 Pro Ile Val His Asn Val Asp

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358 145 150

361 (2) INFORMATION FOR SEQ ID NO: 5:

363 (i) SEQUENCE CHARACTERISTICS:

364 (A) LENGTH: 237 base pairs

365 (B) TYPE: nucleic acid

366 (C) STRANDEDNESS: single

367 (D) TOPOLOGY: linear

369 (ii) MOLECULE TYPE: cDNA

372 (ix) FEATURE:

373 (A) NAME/KEY: CDS

374 (B) LOCATION: 1..237

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/929,612A

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; Xaa Pos.1
Seq#:6; Xaa Pos.1

VERIFICATION SUMMARY

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Input Set : A:\-31-1-5.app

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L:33 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:34 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:381 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:48

L:420 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0